



SEQUENCE LISTING

<110> MACHIDA, Masayuki  
MASAKI, Haruhiko  
KUNIHICO, Sumiko  
HAGIWARA, Hiroko

<120> MARKER FOR SELECTING TRANSFORMANT WITH THE USE OF LETHAL GENE

<130> 040894-7170-US

<140> US 10/522,366

<141> 2005-01-25

<150> PCT/JP03/09543

<151> 2003-07-28

<150> JP 2002-218735

<151> 2002-07-26

<160> 24

<170> PatentIn version 3.4

<210> 1

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<223> Primer

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28

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aaaactgaga atattaaagg gcttggtgat cttaagcctg ggatacaaaa aacaccaaag 120

cagaatggtg gtggaaaacg caagcgttg actggagata aagggcgtaa gatttatgag 180

tgggattctc agcatggtga gcttgagggg tatcgtgccg gtgatggtca gcatcttggc 240

tcatttgacc ctaaaacagg caatcagttg aaaggtccag atccgaaacg aaatatcaag 300

aaatatcttt gaggccatag cggccaagtt atgggactta aattggattt aacttggttt 360

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 gttatagctg aatgggtacc ttgctacaa ccatacttta atcatcaa attgatatttcc 540  
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 <213> Escherichia coli

<400> 9  
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<210> 14

<211> 607

<212> DNA

<213> Escherichia coli

<400> 14

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acaccaaagc agaatggtgg tggaaaacgc aagcgctgga ctggagataa agggcgtaag 180

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tgctttgatg ttatagctga atgggtacct ttgctacaac catactttta tcatcaaatt 540

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<212> DNA

<213> Escherichia coli

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aaggataatg ttaataacgg ttgctttgat gttatagctg aatgggtacc tttgctacaa 180  
ccatacttta atcatcaaat tgatatttcc gataatgagt attttgtttc gtttgattat 240  
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cccgccaaca catcacgggc cacaaaattt tttgtggccc gctctgcgtt ttctaagtgt 180  
tatccctcct gatttctaaa aaattttcca cctgaacttg acagaaaaaa cgatgacgag 240  
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tttgaaatgt cacaaaaatt ccatgtggga gatgggatct aaaatcctcg tgcagaactt 3000
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<210> 17
<211> 551
<212> PRT
<213> Escherichia coli

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<400> 17

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```

Ser Gly Asn Ile Asn Gly Gly Pro Thr Gly Leu Gly Val Gly Gly Gly
          20          25          30

```

```

Ala Ser Asp Gly Ser Gly Trp Ser Ser Glu Asn Asn Pro Trp Gly Gly
          35          40          45

```

```

Gly Ser Gly Ser Gly Ile His Trp Gly Gly Gly Ser Gly His Gly Asn
50          55          60

```

```

Gly Gly Gly Asn Gly Asn Ser Gly Gly Gly Ser Gly Thr Gly Gly Asn
65          70          75          80

```

```

Leu Ser Ala Val Ala Ala Pro Val Ala Phe Gly Phe Pro Ala Leu Ser
          85          90          95

```

```

Thr Pro Gly Ala Gly Gly Leu Ala Val Ser Ile Ser Ala Gly Ala Leu
100          105          110

```

```

Ser Ala Ala Ile Ala Asp Ile Met Ala Ala Leu Lys Gly Pro Phe Lys
115          120          125

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```

Phe Gly Leu Trp Gly Val Ala Leu Tyr Gly Val Leu Pro Ser Gln Ile
130          135          140

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```

Ala Lys Asp Asp Pro Asn Met Met Ser Lys Ile Val Thr Ser Leu Pro
145          150          155          160

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Ala Asp Asp Ile Thr Glu Ser Pro Val Ser Ser Leu Pro Leu Asp Lys
          165          170          175

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Ala Thr Val Asn Val Asn Val Arg Val Val Asp Asp Val Lys Asp Glu  
180 185 190

Arg Gln Asn Ile Ser Val Val Ser Gly Val Pro Met Ser Val Pro Val  
195 200 205

Val Asp Ala Lys Pro Thr Glu Arg Pro Gly Val Phe Thr Ala Ser Ile  
210 215 220

Pro Gly Ala Pro Val Leu Asn Ile Ser Val Asn Asn Ser Thr Pro Ala  
225 230 235 240

Val Gln Thr Leu Ser Pro Gly Val Thr Asn Asn Thr Asp Lys Asp Val  
245 250 255

Arg Pro Ala Gly Phe Thr Gln Gly Gly Asn Thr Arg Asp Ala Val Ile  
260 265 270

Arg Phe Pro Lys Asp Ser Gly His Asn Ala Val Tyr Val Ser Val Ser  
275 280 285

Asp Val Leu Ser Pro Asp Gln Val Lys Gln Arg Gln Asp Glu Glu Asn  
290 295 300

Arg Arg Gln Gln Glu Trp Asp Ala Thr His Pro Val Glu Ala Ala Glu  
305 310 315 320

Arg Asn Tyr Glu Arg Ala Arg Ala Glu Leu Asn Gln Ala Asn Glu Asp  
325 330 335

Val Ala Arg Asn Gln Glu Arg Gln Ala Lys Ala Val Gln Val Tyr Asn  
340 345 350

Ser Arg Lys Ser Glu Leu Asp Ala Ala Asn Lys Thr Leu Ala Asp Ala  
355 360 365

Ile Ala Glu Ile Lys Gln Phe Asn Arg Phe Ala His Asp Pro Met Ala  
370 375 380

Gly Gly His Arg Met Trp Gln Met Ala Gly Leu Lys Ala Gln Arg Ala  
385 390 395 400



Gln Thr Asp Val Asn Asn Lys Gln Ala Ala Phe Asp Ala Ala Ala Lys  
405 410 415

Glu Lys Ser Asp Ala Asp Ala Ala Leu Ser Ser Ala Met Glu Ser Arg  
420 425 430

Lys Lys Lys Glu Asp Lys Lys Arg Ser Ala Glu Asn Asn Leu Asn Asp  
435 440 445

Glu Lys Asn Lys Pro Arg Lys Gly Phe Lys Asp Tyr Gly His Asp Tyr  
450 455 460

His Pro Ala Pro Lys Thr Glu Asn Ile Lys Gly Leu Gly Asp Leu Lys  
465 470 475 480

Pro Gly Ile Pro Lys Thr Pro Lys Gln Asn Gly Gly Gly Lys Arg Lys  
485 490 495

Arg Trp Thr Gly Asp Lys Gly Arg Lys Ile Tyr Glu Trp Asp Ser Gln  
500 505 510

His Gly Glu Leu Glu Gly Tyr Arg Ala Ser Asp Gly Gln His Leu Gly  
515 520 525

Ser Phe Asp Pro Lys Thr Gly Asn Gln Leu Lys Gly Pro Asp Pro Lys  
530 535 540

Arg Asn Ile Lys Lys Tyr Leu  
545 550

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<210> 18
<211> 110
<212> PRT
<213> Escherichia coli
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20 25 30

Lys Gly Leu Gly Asp Leu Lys Pro Gly Ile Pro Lys Thr Pro Lys Gln  
35 40 45

Asn Gly Gly Gly Lys Arg Lys Arg Trp Thr Gly Asp Lys Gly Arg Lys  
50 55 60

Ile Tyr Glu Trp Asp Ser Gln His Gly Glu Leu Glu Gly Tyr Arg Ala  
65 70 75 80

Ser Asp Gly Gln His Leu Gly Ser Phe Asp Pro Lys Thr Gly Asn Gln  
85 90 95

Leu Lys Gly Pro Asp Pro Lys Arg Asn Ile Lys Lys Tyr Leu  
100 105 110

<210> 19  
<211> 97  
<212> PRT  
<213> Escherichia coli

<400> 19

Lys Gly Phe Lys Asp Tyr Gly His Asp Tyr His Pro Ala Pro Lys Thr  
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Glu Asn Ile Lys Gly Leu Gly Asp Leu Lys Pro Gly Ile Pro Lys Thr  
20 25 30

Pro Lys Gln Asn Gly Gly Gly Lys Arg Lys Arg Trp Thr Gly Asp Lys  
35 40 45

Gly Arg Lys Ile Tyr Glu Trp Asp Ser Gln His Gly Glu Leu Glu Gly  
50 55 60

Tyr Arg Ala Ser Asp Gly Gln His Leu Gly Ser Phe Asp Pro Lys Thr  
65 70 75 80

Gly Asn Gln Leu Lys Gly Pro Asp Pro Lys Arg Asn Ile Lys Lys Tyr  
85 90 95

Leu

<210> 20  
<211> 330  
<212> DNA  
<213> Escherichia coli

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caaagcagaa tgggtggtgga aaacgcaagc gctggactgg agataaaggg cgtaagattt 180  
atgagtggga ttctcagcat ggtgagcttg aggggtatcg tgccagtgat ggtcagcatc 240  
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tcaagaaata tctttgaggc catagcggcc 330

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<213> Artificial sequence

<220>  
<223> Synthetic single-stranded oligonucleotide

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<210> 22  
<211> 60  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic single-stranded oligonucleotide

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<212> DNA  
<213> *Saccharomyces cerevisiae*

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gctactctcc caaaacaaa aggtctccgc tgactagggc acatctgaca gaagtggaat 180  
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<210> 24  
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 <212> DNA  
 <213> *Aspergillus oryzae*

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